

SOUTHWEST FISHERIES SCIENCE CENTER
THIRD QUARTER REPORT-FY 2002
For the Period April 1-June 30, 2002

Submitted by: John Hunter, Division Director, Fisheries Resources Division

Title of Accomplishment or Milestone: Produce report on shipboard identification of larval billfish by molecular methods.

Current Status: Manuscript in final stages of preparation (available for review)

Background Information: As part of the new Highly Migratory Species-Fisheries Management Plan (HMS-FMP), the Honolulu and La Jolla NMFS labs have a common interest in describing Essential Fish Habitat (EFH) for billfish spawning and larval development. All six Pacific billfish species occur off Hawaii, the eggs and larvae of most species are either not described or cannot be separated from similar eggs and larvae.

Purpose of Activity: 1) To use molecular DNA approaches to amplify the DNA from billfish larvae captured in net tows and identify them on the basis of restriction length polymorphisms (RFLP's). 2) To do this onboard ship so that adaptive sampling could be used to direct sampling efforts to locate and define areas of high spawning activity.

Description of Accomplishment and Significant Results: In June 2001 a cruise aboard the R/V Townsend Cromwell captured a total of 52 billfish larvae. DNA was extracted from the eye so that the remaining larvae could be used for aging and stomach content analyses. PCR amplifications, restriction enzyme cutting, and gel electrophoretic separations were successfully conducted onboard ship. 51% of the larvae could be identified unambiguously. A manuscript "First shipboard application of a PCR-RFLP protocol to identify billfish larvae at sea in near real-time" is in the final stages of preparation. The authors will be E. Lynn, R. Vetter, M. Musyl and R. Humphreys Jr. The ms will be submitted as a note to Marine Ecology Progress Series.

Significance of Accomplishment: Results confirm the feasibility of at-sea molecular id of billfish larvae. New approaches and new equipment should significantly increase sample throughput and decrease analytical time (currently 12 hours).

Problems: None

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